

(2)

OIPE

## RAW SEQUENCE LISTING

DATE: 08/13/2001

PATENT APPLICATION: US/09/920,671

TIME: 10:48:00

Input Set : A:\RTS-0297 Sequence Listing.txt

Output Set: N:\CRF3\08132001\I920671.raw

ENTERED

p.5

6 <110> APPLICANT: C. Frank Bennett  
7 Susan M. Freier  
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION  
11 <130> FILE REFERENCE: RTS-0297  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/920,671  
C--> 13 <141> CURRENT FILING DATE: 2001-08-01  
13 <160> NUMBER OF SEQ ID NOS: 91  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 20  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence ✓  
21 <220> FEATURE:  
23 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
25 <400> SEQUENCE: 1  
26 tccgtcatcg ctctcaggg 20  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 20  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence ✓  
34 <220> FEATURE:  
36 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
38 <400> SEQUENCE: 2  
39 atgcattctg cccccaagga 20  
42 <210> SEQ ID NO: 3  
43 <211> LENGTH: 1449  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Homo sapiens  
47 <220> FEATURE:  
49 <221> NAME/KEY: CDS  
50 <222> LOCATION: (1)...(1449)  
52 <400> SEQUENCE: 3  
53 atg gtg gag aag ggc ccc gag gtc tca ggg aag cgg aga ggg agg aac 48  
54 Met Val Glu Lys Gly Pro Glu Val Ser Gly Lys Arg Arg Gly Arg Asn  
55 1 5 10 15  
57 aac gcg gcc gcc tcc gcc tcc gcc gcc gcc tcc gcc gcc gcc tcg 96  
58 Asn Ala Ala Ala Ser Ala Ser Ala Ala Ala Ala Ser Ala Ala Ala Ser  
59 20 25 30  
61 gcc gcc tgc gcc tcg cca gcc gcc act gcc gcc tcg ggc gcc gcc gcc 144  
62 Ala Ala Cys Ala Ser Pro Ala Ala Thr Ala Ala Ser Gly Ala Ala Ala  
63 35 40 45  
65 tcc tca gcc tcg gcc gcc gcc gcc tca gcc gcc gcc gcc ccc aat aat 192  
66 Ser Ser Ala Ser Ala Ala Ala Ser Ala Ala Ala Pro Asn Asn  
67 50 55 60  
69 ggc cag aat aaa agt ttg gcg gcg gcg gcc aat ggc aac agc agc 240  
70 Gly Gln Asn Lys Ser Leu Ala Ala Ala Pro Asn Gly Asn Ser Ser  
71 65 70 75 80  
73 agc aac tcc tgg gag gaa ggc agc tcg ggc tcg tcc agc gac gag gag 288

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74 Ser Asn Ser Trp Glu Glu Gly Ser Ser Gly Ser Ser Ser Asp Glu Glu
75                               85                               90                               95
77 cac ggt ggc ggt ggc atg agg gtc gga ccc cag tac cag gcg gtg gtg      336
78 His Gly Gly Gly Gly Met Arg Val Gly Pro Gln Tyr Gln Ala Val Val
79                               100                               105                               110
81 ccc gac ttc gac ccc gcc aaa ctg gca aga cgc agt caa gaa cgg gac      384
82 Pro Asp Phe Asp Pro Ala Lys Leu Ala Arg Arg Ser Gln Glu Arg Asp
83                               115                               120                               125
85 aat ctt ggc atg ttg gtc tgg tca ccc aat caa aat ctg tca gaa gca      432
86 Asn Leu Gly Met Leu Val Trp Ser Pro Asn Gln Asn Leu Ser Glu Ala
87                               130                               135                               140
89 aag ttg gat gaa tac att gcc att gcc aaa gaa aag cat ggg tac aac      480
90 Lys Leu Asp Glu Tyr Ile Ala Ile Ala Lys Glu Lys His Gly Tyr Asn
91 145                               150                               155                               160
93 atg gaa cag gct ctt ggg atg ctc ttc tgg cat aaa cat aat atc gaa      528
94 Met Glu Gln Ala Leu Gly Met Leu Phe Trp His Lys His Asn Ile Glu
95                               165                               170                               175
97 aag tca ttg gct gat ttg ccc aac ttt acc cct ttc cca gat gag tgg      576
98 Lys Ser Leu Ala Asp Leu Pro Asn Phe Thr Pro Phe Pro Asp Glu Trp
99                               180                               185                               190
101 act gtg gaa gat aaa gtc tta ttt gag caa gcc ttt agt ttt cat ggg      624
102 Thr Val Glu Asp Lys Val Leu Phe Glu Gln Ala Phe Ser Phe His Gly
103                               195                               200                               205
105 aaa act ttt cat aga atc caa caa atg ctt cca gat aaa tct ata gca      672
106 Lys Thr Phe His Arg Ile Gln Gln Met Leu Pro Asp Lys Ser Ile Ala
107                               210                               215                               220
109 agt ctg gtg aaa ttt tac tat tct tgg aag aag acg agg act aaa act      720
110 Ser Leu Val Lys Phe Tyr Tyr Ser Trp Lys Lys Thr Arg Thr Lys Thr
111 225                               230                               235                               240
113 agt gtg atg gat cgc cat gcc cgg aaa caa aaa cgg gag cgg gag gag      768
114 Ser Val Met Asp Arg His Ala Arg Lys Gln Lys Arg Glu Arg Glu Glu
115                               245                               250                               255
117 agc gag gat gaa ctg gaa gag gca aat gga aac aat ccc att gac att      816
118 Ser Glu Asp Glu Leu Glu Glu Ala Asn Gly Asn Asn Pro Ile Asp Ile
119                               260                               265                               270
121 gag gtt gat caa aac aag gaa agc aaa aag gag gtt ccc cct act gag      864
122 Glu Val Asp Gln Asn Lys Glu Ser Lys Lys Glu Val Pro Pro Thr Glu
123                               275                               280                               285
125 aca gtt cct cag gtc aaa aaa gaa aaa cat agc aca caa gct aaa aat      912
126 Thr Val Pro Gln Val Lys Lys Glu Lys His Ser Thr Gln Ala Lys Asn
127                               290                               295                               300
129 aga gca aaa agg aaa cct cca aaa gga atg ttt ctt tct caa gaa gat      960
130 Arg Ala Lys Arg Lys Pro Pro Lys Gly Met Phe Leu Ser Gln Glu Asp
131 305                               310                               315                               320
133 gtg gag gct gtt tct gcc aat gcc act gct gct acc acg gtg ctg aga      1008
134 Val Glu Ala Val Ser Ala Asn Ala Thr Ala Ala Thr Thr Val Leu Arg
135                               325                               330                               335
137 caa cta gac atg gaa ttg gtt tca gtc aaa cga cag atc cag aat att      1056
138 Gln Leu Asp Met Glu Leu Val Ser Val Lys Arg Gln Ile Gln Asn Ile

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```

139          340          345          350
141 aaa cag aca aac agt gct ctc aaa gaa aaa ctt gat ggt gga ata gaa 1104
142 Lys Gln Thr Asn Ser Ala Leu Lys Glu Lys Leu Asp Gly Gly Ile Glu
143          355          360          365
145 cca tat cga ctt cca gag gtc att cag aaa tgt aat gca cgt tgg act 1152
146 Pro Tyr Arg Leu Pro Glu Val Ile Gln Lys Cys Asn Ala Arg Trp Thr
147          370          375          380
149 aca gaa gag cag ctt ctc gcc gta caa gcc atc agg aaa tat ggc cga 1200
150 Thr Glu Glu Gln Leu Leu Ala Val Gln Ala Ile Arg Lys Tyr Gly Arg
151 385          390          395          400
153 gat ttt cag gca atc tca gac gtg att ggg aac aaa tca gtg gta caa 1248
154 Asp Phe Gln Ala Ile Ser Asp Val Ile Gly Asn Lys Ser Val Val Gln
155          405          410          415
157 gtg aaa aac ttt ttt gta aat tat cga cgc cgc ttc aac ata gat gaa 1296
158 Val Lys Asn Phe Phe Val Asn Tyr Arg Arg Arg Phe Asn Ile Asp Glu
159          420          425          430
161 gtt tta caa gaa tgg gag gca gaa cat ggt aaa gaa gag acc aat ggg 1344
162 Val Leu Gln Glu Trp Glu Ala Glu His Gly Lys Glu Glu Thr Asn Gly
163          435          440          445
165 ccc agt aac cag aag cct gtg aag tcc cca gat aat tcc att aag atg 1392
166 Pro Ser Asn Gln Lys Pro Val Lys Ser Pro Asp Asn Ser Ile Lys Met
167          450          455          460
169 ccc gaa gag gaa gac gag gct cct gtt ctg gat gtc aga tat gca tct 1440
170 Pro Glu Glu Glu Asp Glu Ala Pro Val Leu Asp Val Arg Tyr Ala Ser
171 465          470          475          480
173 gcc tcc tga 1449
174 Ala Ser
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 23
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence ✓
183 <220> FEATURE:
185 <223> OTHER INFORMATION: PCR Primer ✓
187 <400> SEQUENCE: 4
188 acaatcccat tgacattgag gtt 23
191 <210> SEQ ID NO: 5
192 <211> LENGTH: 26
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence ✓
196 <220> FEATURE:
198 <223> OTHER INFORMATION: PCR Primer ✓
200 <400> SEQUENCE: 5
201 ttgctctat ttttagcttg tgtgct 26
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 30
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence ✓
209 <220> FEATURE:
211 <223> OTHER INFORMATION: PCR Probe ✓

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213 <400> SEQUENCE: 6
214 aaggagggttc cccctactga gacagttcct
217 <210> SEQ ID NO: 7
218 <211> LENGTH: 19
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence ✓
222 <220> FEATURE:
224 <223> OTHER INFORMATION: PCR Primer ✓
226 <400> SEQUENCE: 7
227 gaaggtgaag gtcggagtc
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence ✓
235 <220> FEATURE:
237 <223> OTHER INFORMATION: PCR Primer ✓
239 <400> SEQUENCE: 8
240 gaagatggtg atgggatttc
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 20
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence ✓
248 <220> FEATURE:
250 <223> OTHER INFORMATION: PCR Probe ✓
252 <400> SEQUENCE: 9
253 caagcttccc gttctcagcc
256 <210> SEQ ID NO: 10
257 <211> LENGTH: 5241
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
263 <400> SEQUENCE: 10
264 ggcagctcgg gctcgtccag cgacgaggag cacggtggcg gtggcatgag ggtcggaccc 60
266 cagtaccagg cggtggtgcc cgacttcgac cccgccaaac tggcaagacg cagtcaagaa 120
268 cgggacaatc ttggcatggt ggtctggtca cccaatcaaa atctgtcaga agcaaagtgt 180
270 gatgaataca ttgccattgc caaagaaaag catgggtaca acatggaaca ggctcttggg 240
272 atgctcttct ggcataaaca taatatcgaa aagtcattgg ctgatttgcc caactttacc 300
274 cctttcccag atgagtggac tgtggaagat aaagtcttat ttgagcaagc ctttagtttt 360
276 catgggaaaa cttttcatag aatccaacaa atgcttccag ataaatctat agcaagtctg 420
278 gtgaaatttt actattcttg gaagaagacg aggactaaaa ctagtgtgat ggatcgccat 480
280 gcccggaaac aaaaacggga gcgggaggag agcgaggatg aactggaaga ggcaaatgga 540
282 aacaatccca ttgacattga ggttgatcaa aacaaggaaa gcaaaaagga ggttccccct 600
284 actgagacag ttccctcaggt caaaaaagaa aaacatagca cacaagctaa aaatagagca 660
286 aaaaggaaac ctccaaaagg aatgtttctt tctcaagaag atgtggaggc tgtttctgcc 720
288 aatgccactg ctgctaccac ggtgctgaga caactagaca tgggaattggt ttcagtcaaa 780
290 cgacagatcc agaataattaa acagacaaac agtgctctca aagaaaaact tgatggtgga 840
292 atagaaccat atcgacttcc agaggtcatt cagaaatgta atgcacgttg gactacagaa 900
294 gagcagcttc tcgcctgata agccatcagg aaatatggcc gagattttca ggcaatctca 960
296 gacgtgattg ggaacaaatc agtgggtacaa gtgaaaaact tttttgtaaa ttatcgacgc 1020

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298 cgcttcaaca tagatgaagt tttacaagaa tgggaggcag aacatggtaa agaagagacc 1080
300 aatgggcccc gtaaccagaa gcctgtgaag tccccagata attccattaa gatgcccga 1140
302 gaggaagacg aggtcctgt tctggatgtc agatatgcat ctgcctcctg agaaactgg 1200
304 ggctttgaac acttgggtgt gactactgtg ttatccggga taccaggtat tatgagacat 1260
306 cacctagcca tctgcatcac atctctctgg acaagcagct attacaaaaa aaggcatata 1320
308 cttccagtc tgtgtccat ctgccttaat tctttgtctg ttcttccatg ttggcgccac 1380
310 ttcccagaga gctccactgc atctcacact ctgcccacgt gctggggaag tctcacggcc 1440
312 tgcacatctc ttgtgactct gggaaccgcc tctccgcg gagccccga gccccaccaa 1500
314 tggcagctct tcccagtcag cagcttcaga gcaggcagtc tccttggaag gcccgaactc 1560
316 gttcctgcat ggctgcagt ttctactttg tgcataagat cattttcaga gtcaccgcga 1620
318 cctgtttggc cttctagaaa gtttcttttg ttctttctg agacaaccac ctaagtata 1680
320 atacgctttt ttggaaacta atatatattg ccagactgca tcataacctt tatcatgcca 1740
322 agcatcctga tgcactcac atttccctaa acatggggta cagttatgat ttataaattg 1800
324 agttggctta aatctccctc ttctcccttc ccaagtgtta caaagatcat ttactgcaac 1860
326 tgtcgttggc cactgtagct taaagggaa gtggacctca atgctttctg cttcaactt 1920
328 ttcagcattg tgaccccagg gtggttgcca cccatcttt tctgacccc ccccccccc 1980
330 ccacctccaa gaggttcggc ccacatcact gtacctgggt cttgtaaatt tggatttgt 2040
332 gccttctcct ttgggcaacc atggttatca atccttttc tgttttagtg tcttattct 2100
334 tctttcaagt tatttgctag ccaaagatga catcactgag attaggagac aggggagagc 2160
336 ttgctgcaga ttctgacagt gcagatttta aatgtcagga tattagaata gctggcgctg 2220
338 gtttatgaaa gctgcgcgtt gttccgcgtt ctctcgggtg gcctggcctt ttatgtggca 2280
340 ctctgtatgt cagtttgtgt cttcatgtg ctgatgtgat tacacaaaca ccatgcactc 2340
342 tcttttcata tcagagtaca ggacagagaa gtgatcaatg tattggtota gtgagactga 2400
344 gatgaaaaga aataacctac agagtgtct gtaatgcctt ttggttgga tgggaacaag 2460
346 taaaaatttc taataaacat tttgagactt ccagaatcac tttgtttatc ttatcagacc 2520
348 atgggcctgc tgaggggtga gcagacagcc tgcattctaa cataccctgt tccccccca 2580
350 cggccattca gactgcactc aatacgtga agtcgctttt gttgttggtg ttgttggttg 2640
352 catcatttgg atttttttcc tgccttcaat accaaaaaaa tgcagatgct ttaaggccta 2700
354 aacagaattc tgaagaattt aaaatatgca attaaagttt gatatgtttt gtctcccaag 2760
356 caccttgttt ttgttggttg ttgttggtgt tgaagtcagc tgattttctc tttagaaaga 2820
358 gggtcagcta gaaacctagg ttttttgga ttgtaaattt ttttttagta tagtctggag 2880
360 agaaaggtea ttcaaaagga aagtacaatg ggacttgctg ccttcatca tctcgttccc 2940
362 gtgccagggt tgtgttggtc acgtaaaagc ctgggaagca tcagaggagt cccggattgc 3000
364 tgctgtacc tggagacagg gttagcaaaa taacactagt gatgaggag aggttcttt 3060
366 tcaccataag cctgctgtgt acaccgagg cggcaggaga agcatggga ggagtcagcc 3120
368 taagtttgca cattgcataa agggtaact aaggtagag ctgaagcttt aggttctcg 3180
370 tgcttccctc aagacctcct tctgtctaac agaagcagta ggcaattgct gcagtgcgtt 3240
372 tctcaccctg ccaataggte tgtctgtatc tctgttaagg aaaatagcct ggtccctcct 3300
374 ggcagtgcct ggaagcttga tgctaatttt tatatagcgt ggcaaactga ccagcagtgc 3360
376 caggccttga tctgtattct gcactatccc tttacttggt tcttggaact gaatggtctc 3420
378 cagccctgaa gaatcacgtg tgatcacagc agctgacctg ggctttctcc ccgagaggaa 3480
380 ggggcatgtc atttttattt gacagaggga aataggagc tgccttgac tgcctttgtt 3540
382 gtgctttccc gcgtaagata gcactgtgtt ttaactggtt gcattacact gtctttgcaa 3600
384 tgatgtaaat gtaagaaatc acttagcttt aaaagcgcag tggtttgatc ttatttatat 3660
386 gaagactttt taacatatca agaattaggt gcattggcag gtagggtttg ggggtgtgata 3720
388 actgcttcag atggaatgtt cacttaagct ttgtcttctt aaaaattatc aatgtgaatg 3780
390 tcataattat atatatattt gtggaaaatt ttctcctaag tataagttat tgtgcaaat 3840
392 atagtgtcat tgatgcaaat aatagtttaa ctttttagtt agaactccta aaagatataa 3900
394 attgtattgc atatgcatta aaagtttggt ttatttaatt ttatgtagat gtgtgaagtg 3960

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:2801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12